RAW SEQUENCE LISTING DATE: 07/16/2001
PATENT APPLICATION: **US/09/508,418A** TIME: 11:55:11

Input Set : **A:\Q58140 sequence listing.txt**
Output Set: **N:\CRF3\07162001\I508418A.raw**

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      3 <110> APPLICANT: Nihon Nohyaku Co., Ltd.
      5 <120> TITLE OF INVENTION: NOVEL PROTOPORPHYRINOGEN OXIDASE TOLERANT TO PHOTOBLEACING
HERBICIDE
      7 <130> FILE REFERENCE: Q58140
      9 <140> CURRENT APPLICATION NUMBER: 09/508,418A
C--> 10 <141> CURRENT FILING DATE: 2000-06-08
     12 <150> PRIOR APPLICATION NUMBER: JP 9-265084
     13 <151> PRIOR FILING DATE: 1997-09-11
     15 <160> NUMBER OF SEQ ID NOS: 11
     17 <170> SOFTWARE: PatentIn version 3.0
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 1874
     21 <212> TYPE: DNA
     22 <213> ORGANISM: Nicotiana tabacum
     24 <220> FEATURE:
     25 <221> NAME/KEY: exon
     26 <222> LOCATION: (26)..(1672)
     28 <220> FEATURE:
     29 <221> NAME/KEY: misc_feature
     30 <223> OTHER INFORMATION: Strain name: Xanthi NC
     33 <400> SEQUENCE: 1
     34 agcgcggtct acaagtcagg cagtc atg aca aca act ccc atc gcc aat cat      52
     35                           Met Thr Thr Thr Pro Ile Ala Asn His
     36                           1               5
     38 cct aat att ttc act cac cag tcg tcg tca tcg cca ttg gca ttc tta     100
     39 Pro Asn Ile Phe Thr His Gln Ser Ser Ser Ser Pro Leu Ala Phe Leu
     40 10                  15                  20                  25
     42 aac cgt acg agt ttc atc cct ttc tct tca atc tcc aag cgc aat agt     148
     43 Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser
     44                 30                  35                  40
     46 gtc aat tgc aat ggc tgg aga aca cga tgc tcc gtt gcc aaa gat tac     196
     47 Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr
     48             45                  50                  55
     50 aca gtt cct tcc tca gcg gtc gac ggc gga ccc gcc gcg gag ctg gac     244
     51 Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp
     52         60                  65                  70
     54 tgt gtt ata gtt gga gca gga att agt ggc ctc tgc att gcg cag gtg     292
     55 Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val
     56     75                  80                  85
     58 atg tcc gct aat tac ccc aat ttg atg gta acc gag gcg aga gat cgt     340
     59 Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg
     60 90                  95                  100                 105
     62 gcc ggt ggc aac ata acg act gtg gaa aga gac ggc tat ttg tgg gaa     388
     63 Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu
     64                 110                 115                 120
     66 gaa ggt ccc aac agt ttc cag ccg tcc gat cct atg ttg act atg gca     436
     67 Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Ala
     68             125                 130                 135
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70 gta gat tgt gga ttg aag gat gat ttg gtg ttg gga gat cct aat gcg      484
71 Val Asp Cys Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Asn Ala
72         140                 145                 150
74 ccc cgt ttc gtt ttg tgg aag ggt aaa tta agg ccc gtc ccc tca aaa      532
75 Pro Arg Phe Val Leu Trp Lys Gly Lys Leu Arg Pro Val Pro Ser Lys
76     155                 160                 165
78 ctc act gat ctt ccc ttt ttt gat ttg atg agc att cct ggc aag ttg      580
79 Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Pro Gly Lys Leu
80 170                 175                 180                 185
82 aga gct ggt ttt ggt ccc att ggc ctc cgc cct tca cct cca ggt cat      628
83 Arg Ala Gly Phe Gly Pro Ile Gly Leu Arg Pro Ser Pro Pro Gly His
84                 190                 195                 200
86 gag gaa tca gtt gag cag ttc gtg cgt cgt aat ctt ggt ggc gaa gtc      676
87 Glu Glu Ser Val Glu Gln Phe Val Arg Arg Asn Leu Gly Gly Glu Val
88             205                 210                 215
90 ttt gaa cgc ttg ata gaa cca ttt tgt tct ggt gtt tat gct ggt gat      724
91 Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp
92         220                 225                 230
94 ccc tca aaa ctg agt atg aaa gca gca ttt ggg aaa gtt tgg aag ttg      772
95 Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu
96     235                 240                 245
98 gaa gaa act ggt ggt agc att att gga gga acc ttt aaa gca ata aag      820
99 Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Lys
100 250                 255                 260                 265
102 gag aga tcc agt aca cct aaa gcg ccc cgc gat ccg cgt tta cct aaa      868
103 Glu Arg Ser Ser Thr Pro Lys Ala Pro Arg Asp Pro Arg Leu Pro Lys
104                 270                 275                 280
106 cca aaa gga cag aca gtt gga tca ttc agg aag ggt ctc aga atg ctg      916
107 Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu
108             285                 290                 295
110 ccg gat gca atc agt gca aga ttg gga agc aaa tta aaa cta tca tgg      964
111 Pro Asp Ala Ile Ser Ala Arg Leu Gly Ser Lys Leu Lys Leu Ser Trp
112         300                 305                 310
114 aag ctt tct agc att act aag tca gaa aaa gga gga tat cac ttg aca     1012
115 Lys Leu Ser Ser Ile Thr Lys Ser Glu Lys Gly Gly Tyr His Leu Thr
116     315                 320                 325
118 tac gag aca cca gaa gga gta gtt tct ctt caa agt cga agc att gtc     1060
119 Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Ser Arg Ser Ile Val
120 330                 335                 340                 345
122 atg act gtg cca tcc tat gta gca agc aac ata tta cgt cct ctt tcg     1108
123 Met Thr Val Pro Ser Tyr Val Ala Ser Asn Ile Leu Arg Pro Leu Ser
124                 350                 355                 360
126 gtt gcc gca gca gat gca ctt tca aat ttc tac tat ccc cca gtt gga     1156
127 Val Ala Ala Ala Asp Ala Leu Ser Asn Phe Tyr Tyr Pro Pro Val Gly
128             365                 370                 375
130 gca gtc aca att tca tat cct caa gaa gct att cgt gat gag cgt ctg     1204
131 Ala Val Thr Ile Ser Tyr Pro Gln Glu Ala Ile Arg Asp Glu Arg Leu
132         380                 385                 390
134 gtt gat ggt gaa cta aag gga ttt ggg cag ttg cat cca cgt aca cag     1252
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```
135 Val Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln
136     395                 400                 405
138 gga gtg gaa aca cta gga acg ata tat agt tca tca ctc ttc cct aac     1300
139 Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn
140 410                 415                 420                 425
142 cgt gcc cca aaa ggt cgg gtg cta ctc ttg aac tac att gga gga gca     1348
143 Arg Ala Pro Lys Gly Arg Val Leu Leu Leu Asn Tyr Ile Gly Gly Ala
144                 430                 435                 440
146 aaa aat cct gaa att ttg tct aag acg gag agc caa ctt gtg gaa gta     1396
147 Lys Asn Pro Glu Ile Leu Ser Lys Thr Glu Ser Gln Leu Val Glu Val
148             445                 450                 455
150 gtt gat cgt gac ctc aga aaa atg ctt ata aaa ccc aaa gct caa gat     1444
151 Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Lys Ala Gln Asp
152         460                 465                 470
154 cct ctt gtt gtg ggt gtg cga gta tgg cca caa gct atc cca cag ttt     1492
155 Pro Leu Val Val Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe
156     475                 480                 485
158 ttg gtt ggt cat ctg gat acg cta agt act gca aaa gct gct atg aat     1540
159 Leu Val Gly His Leu Asp Thr Leu Ser Thr Ala Lys Ala Ala Met Asn
160 490                 495                 500                 505
162 gat aat ggg ctt gaa ggg ctg ttt ctt ggg ggt aat tat gtg tca ggt     1588
163 Asp Asn Gly Leu Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ser Gly
164                 510                 515                 520
166 gta gca ttg ggg agg tgt gtt gaa ggt gct tat gaa gtt gca tcc gag     1636
167 Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Val Ala Ser Glu
168             525                 530                 535
170 gta aca gga ttt ctg tct cgg tat gca tac aaa tga aacctgtgtt          1682
171 Val Thr Gly Phe Leu Ser Arg Tyr Ala Tyr Lys
172         540                 545
174 gggggtagtc caaaccttgt tagtagtacg atcatgcctt gggaaaattg gcatgtgcct   1742
176 aaaagttttg ctcattagag ttattttagc cttggtaaat gatttgtact tgatatcagt   1802
178 cgttttcttt gagataaaat gttcctgttc aggaaatata atgtatatca attttaaaca   1862
180 aaaaaaaaaa aa                                                     1874
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 548
185 <212> TYPE: PRT
186 <213> ORGANISM: Nicotiana tabacum
188 <220> FEATURE:
189 <221> NAME/KEY: misc_feature
190 <223> OTHER INFORMATION: Strain name: SR1
193 <400> SEQUENCE: 2
195 Met Thr Thr Thr Pro Ile Ala Asn His Pro Asn Ile Phe Thr His Gln
196 1               5                   10                  15
198 Ser Ser Ser Ser Pro Leu Ala Phe Leu Asn Arg Thr Ser Phe Ile Pro
199             20                  25                  30
201 Phe Ser Ser Ile Ser Lys Arg Asn Ser Val Asn Cys Asn Gly Trp Arg
202         35                  40                  45
204 Thr Arg Cys Ser Val Ala Lys Asp Tyr Thr Val Pro Ser Ser Ala Val
205     50                  55                  60
```

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```
207 Asp Gly Gly Pro Ala Ala Glu Leu Asp Cys Val Ile Val Gly Ala Gly
208 65                  70                  75                  80
210 Ile Ser Gly Leu Cys Ile Ala Gln Val Met Ser Ala Asn Tyr Pro Asn
211                 85                  90                  95
213 Leu Met Val Thr Glu Ala Arg Asp Arg Ala Gly Gly Asn Ile Thr Thr
214             100                 105                 110
216 Val Glu Arg Asp Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln
217         115                 120                 125
219 Pro Ser Asp Pro Met Leu Thr Met Ala Val Asp Cys Gly Leu Lys Asp
220     130                 135                 140
222 Asp Leu Val Leu Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Lys
223 145                 150                 155                 160
225 Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr Asp Leu Pro Phe Phe
226                 165                 170                 175
228 Asp Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Phe Gly Pro Ile
229             180                 185                 190
231 Gly Leu Arg Pro Ser Pro Pro Gly His Glu Glu Ser Val Glu Gln Phe
232         195                 200                 205
234 Val Arg Arg Asn Leu Gly Gly Glu Val Phe Glu Arg Leu Ile Glu Pro
235     210                 215                 220
237 Phe Cys Ser Gly Val Tyr Val Gly Asp Pro Ser Lys Leu Ser Met Lys
238 225                 230                 235                 240
240 Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Glu Thr Gly Gly Ser Ile
241                 245                 250                 255
243 Ile Gly Gly Thr Phe Lys Ala Ile Lys Glu Arg Ser Ser Thr Pro Lys
244             260                 265                 270
246 Ala Pro Arg Asp Pro Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly
247         275                 280                 285
249 Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Asp Ala Ile Ser Ala Arg
250     290                 295                 300
252 Leu Gly Ser Lys Leu Lys Leu Ser Trp Lys Leu Ser Ser Ile Thr Lys
253 305                 310                 315                 320
255 Ser Glu Lys Gly Gly Tyr His Leu Thr Tyr Glu Thr Pro Glu Gly Val
256                 325                 330                 335
258 Val Ser Leu Gln Ser Arg Ser Ile Val Met Thr Val Pro Ser Tyr Val
259             340                 345                 350
261 Ala Ser Asn Ile Leu Arg Pro Leu Ser Val Ala Ala Ala Asp Ala Leu
262         355                 360                 365
264 Ser Asn Phe Tyr Tyr Pro Pro Val Gly Ala Val Thr Ile Ser Tyr Pro
265     370                 375                 380
267 Gln Glu Ala Ile Arg Asp Glu Arg Leu Val Asp Gly Glu Leu Lys Gly
268 385                 390                 395                 400
270 Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val Glu Thr Leu Gly Thr
271                 405                 410                 415
273 Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Lys Gly Arg Val
274             420                 425                 430
276 Leu Leu Leu Asn Tyr Ile Gly Gly Ala Lys Asn Pro Glu Ile Leu Ser
277         435                 440                 445
279 Lys Thr Glu Ser Gln Leu Val Glu Val Val Asp Arg Asp Leu Arg Lys
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```
280     450                 455                 460
282 Met Leu Ile Lys Pro Lys Ala Gln Asp Pro Leu Val Val Gly Val Arg
283 465                 470                 475                 480
285 Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Thr
286                 485                 490                 495
288 Leu Ser Thr Ala Lys Ala Ala Met Asn Asp Asn Gly Leu Glu Gly Leu
289             500                 505                 510
291 Phe Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val
292         515                 520                 525
294 Glu Gly Ala Tyr Glu Val Ala Ser Glu Val Thr Gly Phe Leu Ser Arg
295     530                 535                 540
297 Tyr Ala Tyr Lys
298 545
300 <210> SEQ ID NO: 3
301 <211> LENGTH: 1874
302 <212> TYPE: DNA
303 <213> ORGANISM: Nicotiana tabacum
305 <220> FEATURE:
306 <221> NAME/KEY: exon
307 <222> LOCATION: (26)..(1672)
309 <220> FEATURE:
310 <221> NAME/KEY: misc_feature
311 <223> OTHER INFORMATION: Strain name: SR1
314 <400> SEQUENCE: 3
315 agcgcggtct acaagtcagg cagtc atg aca aca act ccc atc gcc aat cat      52
316                           Met Thr Thr Thr Pro Ile Ala Asn His
317                           1               5
319 cct aat att ttc act cac cag tcg tcg tca tcg cca ttg gca ttc tta     100
320 Pro Asn Ile Phe Thr His Gln Ser Ser Ser Ser Pro Leu Ala Phe Leu
321 10                  15                  20                  25
323 aac cgt acg agt ttc atc cct ttc tct tca atc tcc aag cgc aat agt     148
324 Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser
325                 30                  35                  40
327 gtc aat tgc aat ggc tgg aga aca cga tgc tcc gtt gcc aaa gat tac     196
328 Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr
329             45                  50                  55
331 aca gtt cct tcc tca gcg gtc gac ggc gga ccc gcc gcg gag ctg gac     244
332 Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp
333         60                  65                  70
335 tgt gtt ata gtt gga gca gga att agt ggc ctc tgc att gcg cag gtg     292
336 Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val
337     75                  80                  85
339 atg tcc gct aat tac ccc aat ttg atg gta acc gag gcg aga gat cgt     340
340 Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg
341 90                  95                  100                 105
343 gcc ggt ggc aac ata acg act gtg gaa aga gac ggc tat ttg tgg gaa     388
344 Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu
345                 110                 115                 120
347 gaa ggt ccc aac agt ttc cag ccg tcc gat cct atg ttg act atg gca     436
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VERIFICATION SUMMARY DATE: 07/16/2001
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date